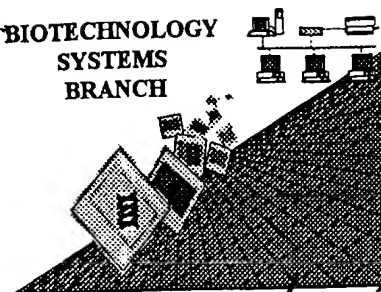


A. Wang

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



Applicant

#6
AW

The Biotechnology Systems Branch of the Scientific and Technical Information Center... (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/978,635

Art Unit / Team No. : 1635

Date Processed by STIC: 8/18/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7.

Other: _____

Applicant must provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

03/973,635

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☒ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.
- 7 ☐ Wrong Designation Sequence(s) ☐ contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of N's or Xaa's (NEW RULES) Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)
- 13 ☐ Wrong Format File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the "Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures" Federal Register Notice, Vol. 63, No. 104, June 1, 1998, p. 29620 applies to applications filed on or after July 1, 1998.
AKS-Biotechnology Systems Branch- 7/10/98

RAW SEQUENCE LISTING

PATENT APPLICATION US/08/978,635

DATE: 08/20/98
TIME: 15:26:08

INPUT SET: S28157.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

(1) General Information

(i) APPLICANTS: ELAZAR RABBANI
JANNIS G. STAVRIANOPOULOS
JAMES J. DONEGAN
DAKAI LIU
NORMAN E. KELKER
DEAN L. ENGELHARDT

(ii) TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING (COMPOSIT

(iii) NUMBER OF SEQUENCES: 42 *delete - just use 42*

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ENZO THERAPEUTICS, INC.
(B) STREET: C/O ENZO BIOCHEM, INC.
527 MADISON AVENUE, 9TH FLOOR
(C) CITY: NEW YORK
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Micro Floppy Disk. 1.44 KB
STORAGE
(B) COMPUTER: IBM PC/XT/AT, IBM PS/2 OR COMPATIBLES
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: MICROSOFT WORD - ASCII TEXT (DOS)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/978,635
(B) FILING DATE: 25-NOVEMBER-1997

(C) CLASSIFICATION: Not Yet Known

(vii) ATTORNEY/AGENT INFORMATION

(A) NAME: FEDUS, RONALD C.
(B) REGISTRATION NUMBER: 32,567
(C) REFERENCE/DOCKET NUMBER: ENZ-53(D4)

(viii) TELECOMMUNICATION INFORMATION

(A) TELEPHONE: (212) 583-0100
(B) TELEFAX: (212) 583-0150

*Don't know
what to do about this*

*error
throughout*

all items 3

*on Enzo
summary
sheet*

Release

*adjust line
every 4 globally*

*Re sequence files,
only 72 classes
per line allowed*

fix mayhem

-->

--> OK

INPUT SET: S28157.raw

--> 46 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:1:
47

delete

ERRORED SEQUENCES FOLLOW:

*(see 1822h)
Per sequence Rel., and one
space between amino acids*

--> 48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) ~~LENGTH:20~~ amino acids
52 (B) TYPE:amino acid
53 (C) STRANDEDNESS:single
54 (D) TOPOLOGY:linear
55
56 (ii) MOLECULE TYPE: peptide
57
58 (iii) HYPOTHETICAL: NO
59 *(X) L- fix globally*
60 ~~(ix)~~ SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62 Gly Phe Phe Gly Ala Ile Ala Gly Phe Leu Glu Gly Gly Trp
63 ~~21~~ 5 10 10
64
65 Met Ile Ala Gly
66 ~~20~~ 20
67
68

*only 18 visible on page**If amino numbering.
Do NOT use TAB codes between
amino numbers. Use space character.*

--> 813 (2) INFORMATION FOR SEQ ID NO:42:
814
815 (i) SEQUENCE CHARACTERISTICS:
816 (A) LENGTH:67 base pairs
817 (B) TYPE:nucleic acid
818 (C) STRANDEDNESS:single
819 (D) TOPOLOGY:linear
820
821 (ii) MOLECULE TYPE: other nucleic acid
822 (A) DESCRIPTION: /desc = "oligonucleotide"
823
824 (iii) HYPOTHETICAL: YES
825 *(X)*
826 ~~(ix)~~ SEQUENCE DESCRIPTION: SEQ ID NO:42:
827
828 CCGGATAATA CGACTCACTA TAGGGCGAGC TCGGTACCCG GGTCTAGAGT CGACCTGCAG 60
829
830 GCATGCT 67
831
832
833
834
835

see next page

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/978,635*

DATE: 08/20/98
TIME: 15:26:10

INPUT SET: S28157.raw

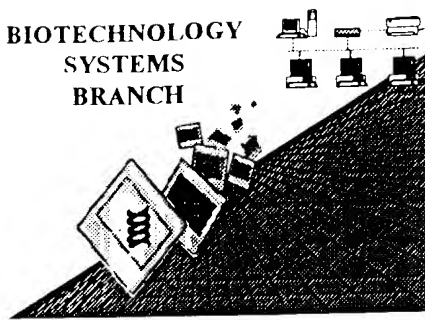
836 LC/WORD/USPROSECUTION/ENZ53D4/SEQUENCE LISTING.060898..enz-53(D4)
--> 837 **SEQ ID: PAGE 15**
838
839 ENZ-53(D4)
840
841 ENZ-53(D4)
842
843
844

delete

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/978,635DATE: 08/20/98
TIME: 15:26:10

INPUT SET: S28157.raw

Line	Error	Original Text
14	Number of Sequences (0) Doesn't Equal Actual Count (42)	(iii)NUMBER OF SEQUENCES: __42__
35	Wrong Classification	(C)CLASSIFICATION:Not Yet Known
46	Unknown or Misplaced Identifier	(ix)SEQUENCE DESCRIPTION:SEQ ID NO:1:
51	Entered (20) and Calc. Seq. Length (19) differ	(A)LENGTH:20 amino acids
816	Entered (67) and Calc. Seq. Length (71) differ	(A)LENGTH:67 base pairs
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	Wrong Nucleic Acid Designator	SEQ ID: PAGE 15
837	# of Sequences for line conflicts w/ running total	SEQ ID: PAGE 15



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: `pub/checker/`
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
WASHINGTON DC 20231

COST FOR DISKETTE IS **\$ 25.00**

METHOD OF PAYMENT:

Check payable to Commissioner of Patents and Trademarks
VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
PTO Deposit Account

For Further Information, Contact: **Arti Shah at 703-308-4212**